

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: JULIUS, Michael H.; FILIPP, Dominik;
ALIZADEH-KHIAVI, Kamel

(ii) TITLE OF INVENTION: BOVINE LACTATION ASSOCIATED IMMUNOTROPIC
PROTEIN (CD14), ENCODING GENE AND
APPLICATION
IN B CELL ACTIVATION

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Torys LLP (Customer No. 33721)
(B) STREET: Suite 3000, 79 Wellington Street West, Box 270
(C) CITY: Toronto
(D) PROVINCE: Ontario
(E) COUNTRY: Canada
(F) ZIP: M5K 1N2

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
(B) COMPUTER: COMPAQ, IBM PC compatible
(C) OPERATING SYSTEM: MS-DOS 5.1
(D) SOFTWARE: WORD PERFECT

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/313,177
(B) FILING DATE: May 18, 1999

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBERS: 08/746,883; PCT/CA 97/00880
(B) FILING DATE: November 18, 1996; November 18, 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hunt, John C.
(B) REGISTRATION NUMBER: 36,424
(C) REFERENCE/DOCKET NUMBER: 47841/00047

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (416) 863-4344
(B) TELEFAX: (416) 863-2653

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGTGTGCG TGCCCTACCT GCTGCTGCTG CTGCTGCCGT CACTGCTGCG TGTGTCTGCG
60

GACACAACAG AACCTTGCAG GCTGGACGAC GACGATTTCC GTTGTGTCTG CAACTTCACG
120

GATCCGAAGC CTGACTGGTC TAGCGCCGTT CAGTGTATGG TTGCCCTCGA GGTGGAGATC
180

AGTGCCGGCG GCCGCAGCCT GGAACAGTTT CTCAAGGGAG CCGACACCAA CCCGAAGCAG
240

TATGCTGACA CAATCAAGGC TCTGCGCGTT CGGCGACTCA AGCTGGGCGC TGCACAGGTT
300

CCTGCTCAGC TTCTGGTCGC CGTTCTGCCG GCGCTCGGGT ACTCTCGTCT CAAGGAACTG
360

ACGCTTGAGG ACCTGGAGGT AACCGGCCCA ACGCCCCCGA CGCCTCTGGA AGCCGCTGGG
420

CCTGCGCTCA CCACCCTCAG TCTGCGTAAC GTATCGTGGA CAACAGGAGG TGCCTGSCCT
480

GGCGAACTGC AGCAGTGGCT CAAGCCTGGG CTCAGGGTGC TGAACATTGC CCAAGCACAC
540

TCGCTTGCCCT TTCCGTGCGC AGGGCTCTCC ACCTTCGAGG CGCTCACCAC CCTAGACCTG
600

TCTGACAATC CCAGTCTCGG CGACACGGGG CTGATGGCAG CTCTCTGTCC GAACAAGTTC
660

CCGCCCCCTCC AATATCTAGC GCTACGCAAC GCGGGGATGG AGACGCCGAG CGGCGTGTGC
720

GCGGCGCTGG CGGCAGCGAG GGTGCAGCCC CAAAGCCTGG ACCTCAGCCA CAACTCGCTG
780

CGCGTCAACG CCCCCGGTGC TACCCGATGT GTCTGGCCCA GTGACTAAG GTCTCTCAAT
840

TTGTCGTTTC CTGGGCTGGA GCAAGTGCCT AAGGGACTGC CCCCTAAGCT CAGCGTGCTT
900

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GATCTCAGCT GCAACAAGCT AAGCAGGGAG CCGCGGCGAG ACGAGCTGCC CGAGGTAAAT
960

GACCTGACTC TGGACGGAAA TCCCTTTCTG GACCTGGAG CCCTCCAGCA CCAAAATGAC
1020

CCGATGATCT CCGGCGTGGT CCCAGCCTGT GCGCGTTCTG CCTTGACCAT GGGGGTGTCA
1080

GGAGCCCTGG CGCTGCTTCA AGGAGCCCGA GGCTTCGCGT AA
1122

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGGAGCGCG CGTCCTGCTT GTTGCTGCTG CTGCTGCCGC TGGTGACGT CTCTGCGACC
60

ACGCCAGAAC CTTGTGAGCT GGACGATGAA GATTTCGGCT GCGTCTGCAA CTTCTCCGAA
120

CCTCAGCCCG ACTGGTCCGA AGCCTTCCAG TGTGTGTCTG CAGTAGAGGT GGAGATCCAT
180

GGCGGCGGTC TCAACCTAGA GCCGTTTCTA AAGCGCGTCG ATGCGGACGC CGACCCGCGG
240

CAGTATGCTG ACACGGTCAA GGCTCTCCGC GTGCGGCGGC TCACAGTGGG AGCCGCACAG
300

GTCCTGCTC AGCTACTGGT AGGCGCCCTG CGTGTGCTAG CGTACTCCCG CCTCAAGGAA
360

CTGACGCTCG AGGACCTAAA GATAACCGGC ACCATGCCTC CGCTGCCTCT GGAAGCCACA
420

GGACTTGAC TTTCCAGCTT GCGCCTACGC AACGTGTCGT GGGCGACAGG GCGTTCTTGG
480

CTCGCCGAGC TGCAGCAGTG GCTCAAGCCA GGCCTCAAGG TACTGAGCAT TGCCCAAGCA
540

CACTCGCCTG CCTTTTCCTG CGAACAGGTT CGCGCCTTCC CGGCCCTTAC CAGCCTAGAC
600

CTGTCTGACA ATCCTGGACT GGGCGAACGC GGAATGATGG CGGCTCTCTG TCCCCACAAG
660

TTCCCGGCCA TCCAGAATCT AGCGCTGCGC AACACAGGAA TGGAGACGCC CACAGGCGTG
720

TGCGCCGCAC TGGCGGCGGC AGGTGTGCAG CCCCACAGCC TAGACCTCAG CCACAACTCG
780

CTGCCCGCCA CCGTAAACCC TAGCGCTCCG AGATGCATGT GGTCCAGCGC CCTGAACTCC
840

CTCAATCTGT CGTTCGCTGG GCTGGAACAG GTGCCTAAAG GACTGCCAGC CAAGCTCAGA
900

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GTGCTCGATC TCAGCTGCAA CAGACTGAAC AGGGCGCCGC AGCCTGACGA GCTCCCCGAG
960

GTGGATAACC TGACACTGGA CGGGAATCCC TTCTTGGTCC CTGGAACTGC CCTCCCCCAC
1020

GAGGGCTCAA TGAATCCGG CGTGGTCCCA GCCTGTGCAC GTTCGACCCT GTCGGTGGGG
1080

GTGTCGGGAA CCCTGGTGCT GCTCCAAGGG GCCCGGGGCT TTGCCTAA
1128

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(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGAGCGTG TGCTTGGCTT GTTGCTGTTG CTTCTGGTGC ACGCCTCTCC CGCCCCACCA
60

GAGCCCTGCG AGCTAGACGA GGAAAGTTGT TCCTGCAACT TCTCAGATCC GAAGCCAGAT
120

TGGTCCAGCG CTTTCAATTG TTTGGGGGCG GCAGATGTGG AATTGTACGG CGGCGGCCCG
180

AGCCTGGAAT ACCTTCTAAA GCGTGTGGAC ACGGAAGCAG ATCTGGGGCA GTTCACTGAT
240

ATTATCAAGT CTCTGTCCCT AAAGCGGCTT ACGGTGCGGG CCGCGCGGAT TCCTAGTCGG
300

ATTCTATTCC GAGCCCTGCG TGTGCTCGGG ATTTCCGGCC TCCAGGAACT GACTCTTGAA
360

AATCTCGAGG TAACCGGCAC CGCGCCGCCA CCGCTTCTGG AAGCCACCGG ACCCGATCTC
420

AACATCTTGA ACCTCCGCAA CGTGTCTGTT GCAACAAGGG ATGCCTGGCT CGCAGAACTG
480

CAGCAGTGGC TAAAGCCTGG ACTCAAGGTA CTGAGTATTG CCCAAGCACA CTCACTCAAC
540

TTTTCCTGCG AACAGGTCCG CGTCTTCCCT GCCCTCTCCA CCTTAGACCT GTCTGACAA
600

CCTGAATTGG GCGAGAGAGG ACTGATCTCA GCCCTCTGTC CCCTCAAGTT CCCGACCCCT
660

CAAGTTTTAG CGCTGCGTAA CGCGGGGATG GAGACGCCCA GCGGCGTGTG CTCTGCGCTG
720

GCCGCAGCAA GGTACAGCT GCAAGGACTA GACCTTAGTC ACAATTCAC T GCGGGATGCT
780

GCAGGCGCTC CGAGTTGTGA CTGGCCCAGT CAGCTAAACT CGCTCAATCT GTCTTTCACT
840

GGGCTGAAGC AGGTACCTAA AGGGCTGCCA GCCAAGCTCA GCGTGCTGGA TCTCAGTTAC
900

AACAGGCTGG ATAGGAACCC TAGCCCAGAT GAGCTGCCCC AAGTGGGGAA CCTGTCACTT
960

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AAAGGAAATC CCTTTTGGG CTCTGAATCC CACTCGGAGA AGTTTAACTC TGGCGTACTC
1020

ACCGCCGGAG CTCCATCATC CCAAGCAGTG GCCTTGTGAG GAACTCTGGC TTGCTCCTA
1080

GGAGATCGCC TCTTTGTTTA A
1101

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(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Cys	Val	Pro	Tyr	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Ser	Leu	Leu	
1				5					10					15		
Arg	Val	Ser	Ala	Asp	Thr	Thr	Glu	Pro	Cys	Glu	Leu	Asp	Asp	Asp	Asp	
			20					25					30			
Phe	Arg	Cys	Val	Cys	Asn	Phe	Thr	Asp	Pro	Lys	Pro	Asp	Trp	Ser	Ser	
		35				40						45				
Ala	Val	Gln	Cys	Met	Val	Ala	Val	Glu	Val	Glu	Ile	Ser	Ala	Gly	Gly	
	50					55					60					
Arg	Ser	Leu	Glu	Gln	Phe	Leu	Lys	Gly	Ala	Asp	Thr	Asn	Pro	Lys	Gln	
65					70					75					80	
Tyr	Ala	Asp	Thr	Ile	Lys	Ala	Leu	Arg	Val	Arg	Arg	Leu	Lys	Leu	Gly	
				85				90						95		
Ala	Ala	Gln	Val	Pro	Ala	Gln	Leu	Leu	Val	Ala	Val	Leu	Arg	Ala	Leu	
			100					105					110			
Gly	Tyr	Ser	Arg	Leu	Lys	Glu	Leu	Thr	Leu	Glu	Asp	Leu	Glu	Val	Thr	
		115					120					125				
Gly	Pro	Thr	Pro	Pro	Thr	Pro	Leu	Glu	Ala	Ala	Gly	Pro	Ala	Leu	Thr	
	130					135					140					
Thr	Leu	Ser	Leu	Arg	Asn	Val	Ser	Trp	Thr	Thr	Gly	Gly	Ala	Trp	Leu	
145					150					155					160	
Gly	Glu	Leu	Gln	Gln	Trp	Leu	Lys	Pro	Gly	Leu	Arg	Val	Leu	Asn	Ile	
				165					170					175		
Ala	Gln	Ala	His	Ser	Leu	Ala	Phe	Pro	Cys	Ala	Gly	Leu	Ser	Thr	Phe	
			180					185					190			
Glu	Ala	Leu	Thr	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Pro	Ser	Leu	Gly	Asp	
		195					200					205				
Thr	Gly	Leu	Met	Ala	Ala	Leu	Cys	Pro	Asn	Lys	Phe	Pro	Ala	Leu	Gln	
	210					215					220					
Tyr	Leu	Ala	Leu	Arg	Asn	Ala	Gly	Met	Glu	Thr	Pro	Ser	Gly	Val	Cys	
225					230					235					240	

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Ala Ala Leu Ala Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser
 245 250 255
 His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp
 260 265 270
 Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln
 275 280 285
 Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys
 290 295 300
 Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn
 305 310 315 320
 Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln
 325 330 335
 His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg
 340 345 350
 Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly
 355 360 365
 Ala Arg Gly Phe Ala
 370

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Leu Pro Leu Val His
 1 5 10 15
 Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe
 20 25 30
 Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala
 35 40 45
 Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu
 50 55 60
 Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg
 65 70 75 80
 Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val
 85 90 95
 Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val
 100 105 110

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(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Glu	Arg	Val	Leu	Gly	Leu	Leu	Leu	Leu	Leu	Val	His	Ala	Ser	1	5	10	15
Pro	Ala	Pro	Pro	Glu	Pro	Cys	Glu	Leu	Asp	Glu	Glu	Ser	Cys	Ser	Cys	20	25	30
Asn	Phe	Ser	Asp	Pro	Lys	Pro	Asp	Trp	Ser	Ser	Ala	Phe	Asn	Cys	Leu	35	40	45
Gly	Ala	Ala	Asp	Val	Glu	Leu	Tyr	Gly	Gly	Gly	Arg	Ser	Leu	Glu	Tyr	50	55	60
Leu	Leu	Lys	Arg	Val	Asp	Thr	Glu	Ala	Asp	Leu	Gly	Gln	Phe	Thr	Asp	65	70	75
Ile	Ile	Lys	Ser	Leu	Ser	Leu	Lys	Arg	Leu	Thr	Val	Arg	Ala	Ala	Arg	85	90	95
Ile	Pro	Ser	Arg	Ile	Leu	Phe	Gly	Ala	Leu	Arg	Val	Leu	Gly	Ile	Ser	100	105	110
Gly	Leu	Gln	Glu	Leu	Thr	Leu	Glu	Asn	Leu	Glu	Val	Thr	Gly	Thr	Ala	115	120	125
Pro	Pro	Pro	Leu	Leu	Glu	Ala	Thr	Gly	Pro	Asp	Leu	Asn	Ile	Leu	Asn	130	135	140
Leu	Arg	Asn	Val	Ser	Trp	Ala	Thr	Arg	Asp	Ala	Trp	Leu	Ala	Glu	Leu	145	150	155
Gln	Gln	Trp	Leu	Lys	Pro	Gly	Leu	Lys	Val	Leu	Ser	Ile	Ala	Gln	Ala	165	170	175
His	Ser	Leu	Asn	Phe	Ser	Cys	Glu	Gln	Val	Arg	Val	Phe	Pro	Ala	Leu	180	185	190
Ser	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Pro	Glu	Leu	Gly	Glu	Arg	Gly	Leu	195	200	205
Ile	Ser	Ala	Leu	Cys	Pro	Leu	Lys	Phe	Pro	Thr	Leu	Gln	Val	Leu	Ala	210	215	220
Leu	Arg	Asn	Ala	Gly	Met	Glu	Thr	Pro	Ser	Gly	Val	Cys	Ser	Ala	Leu	225	230	235
Ala	Ala	Ala	Arg	Val	Gln	Leu	Gln	Gly	Leu	Asp	Leu	Ser	His	Asn	Ser	245	250	255

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Leu Arg Asp Ala Ala Gly Ala Pro Ser Cys Asp Trp Pro Ser Gln Leu
260 265 270

Asn Ser Leu Asn Leu Ser Phe Thr Gly Leu Lys Gln Val Pro Lys Gly
275 280 285

Leu Pro Ala Lys Leu Ser Val Leu Asp Leu Ser Tyr Asn Arg Leu Asp
290 295 300

Arg Asn Pro Ser Pro Asp Glu Leu Pro Gln Val Gly Asn Leu Ser Leu
305 310 315 320

Lys Gly Asn Pro Phe Leu Asp Ser Glu Ser His Ser Glu Lys Phe Asn
325 330 335

Ser Gly Val Val Thr Ala Gly Ala Pro Ser Ser Gln Ala Val Ala Leu
340 345 350

Ser Gly Thr Leu Ala Leu Leu Leu Gly Asp Arg Leu Phe Val
355 360 365

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCTAGCGCTA GCCACCATGG TGTGCGTGCC CTACCTGCT
39

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTAGCGCTA GCCGCGAAGC CTCGGGCTCC TTGAAG
36

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(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTCGAGCTCG AGGCTAGCCA CCATGGTGTG CGTCCC

36

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGCTGA GGGATCCCTA AGCGTAATCT GGAAC

35

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTAGAATTCT CTCCCGCCCC ACCAGAGCCC TGCG

34

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAGAATTCT TAAACAAAGA GGCGATCTCC TAGG
34

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TACCAATACG ATGTTCCAGA TTACGCTTAG
30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GCAGTCGACA CTATAGAATA CTCAAGC
27

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetic Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TTCGTCGACA TTGGGCCCTC TAGA

24